EXHIBIT 1

Curriculum vitae:

Christian Isak Jørgensen:

1992: Bachelor in Biotechnology;
Department of Molecular Biology,
University of Southern Denmark, Odense

1995: Master in Molecular and Cell Biology;
Department of Molecular Biology,
University of Southern Denmark, Odense

1999: Ph.D. in Molecular Biology;
Department of Molecular Biology,
University of Southern Denmark, Odense

1999: Research Scientist;
Department of Biochemistry and Molecular Biology,
University of Southern Denmark, Odense

2001: Research Scientist at Novozymes

Since June 2001:
Responsible for Mass spectrometry and N-terminal sequencing facilities at Novozymes

2002: Procise sequencing Training;
Applied Biosystems, Langen, Germany

2002: Mass spectrometry Training;
Applied Biosystems, Langen, Germany

2002: Biochrom Systems AAA Training;
Biochrom Ltd, Cambridge, England

EXHIBIT 2

SPEZYME® ETHYL DNA SEQUENCE

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          M  K  Q  Q  K  R  L  Y  A  R  L  L  T  L  L  F  A  L
  1 AGAATCATGA AACAACAAAA ACGGCTTTAC GCCCGATTGC TGACGCTGTT ATTTGCGCTC
    TCTTAGTACT TTGTTGTTTT TGCCGAAATG CGGGCTAACG ACTGCGACAA TAAACGCGAG

          I  F  L  L  P  H  S  A  A  S  A  A  A  P  F  N  G  T  M  M
 61 ATCTTCTTGC TGCCTCATTC TGCAGCTTCA GCAGCCGCAC CGTTTAACGG CACCATGATG
    TAGAAGAACG ACGGAGTAAG ACGTCGAAGT CGTCGGCGTG GCAAATTGCC GTGGTACTAC

          Q  Y  F  E  W  Y  L  P  D  D  G  T  L  W  T  K  V  A  N  E
121 CAGTATTTTG AATGGTACTT GCCGGATGAT GGCACGTTAT GGACCAAAGT GGCCAATGAA
    GTCATAAAAC TTACCATGAA CGGCCTACTA CCGTGCAATA CCTGGTTTCA CCGGTTACTT

          A  N  N  L  S  S  L  G  I  T  A  L  W  L  P  P  A  Y  K  G
181 GCCAACAACT TATCCAGCCT TGGCATCACC GCTCTTTGGC TGCCGCCCGC TTACAAAGGA
    CGGTTGTTGA ATAGGTCGGA ACCGTAGTGG CGAGAAACCG ACGGCGGGCG AATGTTTCCT

          T  S  R  S  D  V  G  Y  G  V  Y  D  L  Y  D  L  G  E  F  N
241 ACAAGCCGCA GCGACGTAGG GTACGGAGTA TACGACTTGT ATGACCTCGG CGAATTCAAT
    TGTTCGGCGT CGCTGCATCC CATGCCTCAT ATGCTGAACA TACTGGAGCC GCTTAAGTTA

          Q  K  G  T  V  R  T  K  Y  G  T  K  A  Q  Y  L  Q  A  I  Q
301 CAAAAAGGGA CCGTCCGCAC AAAATATGGA ACAAAAGCTC AATATCTTCA AGCCATTCAA
    GTTTTTCCCT GGCAGGCGTG TTTTATACCT TGTTTTCGAG TTATAGAAGT TCGGTAAGTT

          A  A  H  A  A  G  M  Q  V  Y  A  D  V  V  F  D  H  K  G  G
361 GCCGCCCACG CCGCTGGAAT GCAAGTGTAC GCCGATGTCG TGTTCGACCA TAAAGGCGGC
    CGGCGGGTGC GGCGACCTTA CGTTCACATG CGGCTACAGC ACAAGCTGGT ATTTCCGCCG

          A  D  G  T  E  W  V  D  A  V  E  V  N  P  S  D  R  N  Q  E
421 GCTGACGGCA CGGAATGGGT GGACGCCGTC GAAGTCAATC CGTCCGACCG CAACCAAGAA
    CGACTGCCGT GCCTTACCCA CCTGCGGCAG CTTCAGTTAG GCAGGCTGGC GTTGGTTCTT

          I  S  G  T  Y  Q  I  Q  A  W  T  K  F  D  F  P  G  R  G  N
481 ATCTCGGGCA CCTATCAAAT CCAAGCATGG ACGAAATTTG ATTTTCCCGG GCGGGGCAAC
    TAGAGCCCGT GGATAGTTTA GGTTCGTACC TGCTTTAAAC TAAAAGGGCC CGCCCCGTTG

          T  Y  S  S  F  K  W  R  W  Y  H  F  D  G  V  D  W  D  E  S
541 ACCTACTCCA GCTTTAAGTG GCGCTGGTAC CATTTTGACG GCGTTGATTG GGACGAAAGC
    TGGATGAGGT CGAAATTCAC CGCGACCATG GTAAAACTGC CGCAACTAAC CCTGCTTTCG

          R  K  L  S  R  I  Y  K  F  I  G  K  A  W  D  W  E  V  D  T
601 CGAAAATTAA GCCGCATTTA CAAATTCATC GGCAAAGCGT GGGATTGGGA AGTAGACACA
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661     GAAAACGGAA ACTATGACTA CTTAATGTAT GCCGACCTTG ATATGGATCA TCCCGAAGTC
        CTTTTGCCTT TGATACTGAT GAATTACATA CGGCTGGAAC TATACCTAGT AGGGCTTCAG

        V  T  E  L   K  N  W   G  K  W   Y  V  N  T   T  N  I   D  G  F
721     GTGACCGAGC TGAAAAACTG GGGGAAATGG TATGTCAACA CAACGAACAT TGATGGGTTC
        CACTGGCTCG ACTTTTTGAC CCCCTTTACC ATACAGTTGT GTTGCTTGTA ACTACCCAAG

        R  L  D  A   V  K  H   I  K  F   S  F  F  P   D  W  L   S  Y  V
781     CGGCTTGATG CCGTCAAGCA TATTAAGTTC AGTTTTTTTC CTGATTGGTT GTCGTATGTG
        GCCGAACTAC GGCAGTTCGT ATAATTCAAG TCAAAAAAAG GACTAACCAA CAGCATACAC

        R  S  Q  T   G  K  P   L  F  T   V  G  E  Y   W  S  Y   D  I  N
841     CGTTCTCAGA CTGGCAAGCC GCTATTTACC GTCGGGGAAT ATTGGAGCTA TGACATCAAC
        GCAAGAGTCT GACCGTTCGG CGATAAATGG CAGCCCCTTA TAACCTCGAT ACTGTAGTTG

        K  L  H  N   Y  I  T   K  T  N   G  T  M  S   L  F  D   A  P  L
901     AAGTTGCACA ATTACATTAC GAAAACAAAC GGAACGATGT CTTTGTTTGA TGCCCCGTTA
        TTCAACGTGT TAATGTAATG CTTTTGTTTG CCTTGCTACA GAAACAAACT ACGGGGCAAT

        H  N  K  F   Y  T  A   S  K  S   G  G  A  F   D  M  R   T  L  M
961     CACAACAAAT TTTATACCGC TTCCAAATCA GGGGGCGCAT TTGATATGCG CACGTTAATG
        GTGTTGTTTA AAATATGGCG AAGGTTTAGT CCCCCGCGTA AACTATACGC GTGCAATTAC

        T  N  T  L   M  K  D   Q  P  T   L  A  V  T   F  V  D   N  H  D
1021    ACCAATACTC TCATGAAAGA TCAACCGACA TTGGCCGTCA CCTTCGTTGA TAATCATGAC
        TGGTTATGAG AGTACTTTCT AGTTGGCTGT AACCGGCAGT GGAAGCAACT ATTAGTACTG

        T  E  P  G   Q  A  L   Q  S  W   V  D  P  W   F  K  P   L  A  Y
1081    ACCGAACCCG GCCAAGCGCT TCAGTCATGG GTCGACCCAT GGTTCAAACC GTTGGCTTAC
        TGGCTTGGGC CGGTTCGCGA AGTCAGTACC CAGCTGGGTA CCAAGTTTGG CAACCGAATG

        A  F  I  L   T  R  Q   E  G  Y   P  C  V  F   Y  G  D   Y  Y  G
1141    GCCTTTATTC TAACTCGGCA GGAAGGATAC CCGTGCGTCT TTTATGGTGA CTATTATGGC
        CGGAAATAAG ATTGAGCCGT CCTTCCTATG GGCACGCAGA AAATACCACT GATAATACCG

        I  P  Q  Y   N  I  P   S  L  K   S  K  I  D   P  L  L   I  A  R
1201    ATTCCACAAT ATAACATTCC TTCGCTGAAA AGCAAAATCG ATCCGCTCCT CATCGCGCGC
        TAAGGTGTTA TATTGTAAGG AAGCGACTTT TCGTTTTAGC TAGGCGAGGA GTAGCGCGCG

        R  D  Y  A   Y  G  T   Q  H  D   Y  L  D  H   S  D  I   I  G  W
1261    AGGGATTATG CTTACGGAAC GCAACATGAT TATCTTGATC ACTCCGACAT CATCGGGTGG
        TCCCTAATAC GAATGCCTTG CGTTGTACTA ATAGAACTAG TGAGGCTGTA GTAGCCCACC
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        T  R  E  G   V  T  E   K  P  G   S  G  L  A   A  L  I   T  D  G
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        TGTTCCCTTC CCCAGTGACT TTTTGGTCCT AGGCCCGACC GGCGTGACTA GTGGCTACCC

        P  G  G  S   K  W  M   Y  V  G   K  Q  H  A   G  K  V   F  Y  D
1381    CCGGGAGGAA GCAAATGGAT GTACGTTGGC AAACAACACG CTGGAAAAGT GTTCTATGAC
        GGCCCTCCTT CGTTTACCTA CATGCAACCG TTTGTTGTGC GACCTTTTCA CAAGATACTG

        L  T  G  N   R  S  D   T  V  T   I  N  S  D   G  W  G   E  F  K
1441    CTTACCGGCA ACCGGAGTGA CACCGTCACC ATCAACAGTG ATGGATGGGG GGAATTCAAA
        GAATGGCCGT TGGCCTCACT GTGGCAGTGG TAGTTGTCAC TACCTACCCC CCTTAAGTTT

        V  N  G  G   S  V  S   V  W  V   P  R  K  T   T  V  S   T  I  A
1501    GTCAATGGCG GTTCGGTTTC GGTTTGGGTT CCTAGAAAAA CGACCGTTTC TACCATCGCT
        CAGTTACCGC CAAGCCAAAG CCAAACCCAA GGATCTTTTT GCTGGCAAAG ATGGTAGCGA

        R  P  I  T   T  R  P   W  T  G   E  F  V  R   W  T  E   P  R  L
1561    CGGCCGATCA CAACCCGACC GTGGACTGGT GAATTCGTCC GTTGGACCGA ACCACGGTTG
        GCCGGCTAGT GTTGGGCTGG CACCTGACCA CTTAAGCAGG CAACCTGGCT TGGTGCCAAC

        V  A  W  P  *
1621    GTGGCATGGC CTTGAGTTAA CAGAGGACGG ATTTCCTGAA GGAAATCCGT TTTTTTATTT
        CACCGTACCG GAACTCAATT GTCTCCTGCC TAAAGGACTT CCTTTAGGCA AAAAAATAAA

1681    TAAG
        ATTC
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EXHIBIT 3

SPEZYME® ETHYL AMINO ACID SEQUENCE

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  1 AAPFNGTMMQ YFEWYLPDDG TLWTKVANEA NNLSSLGITA LWLPPAYKGT SRSDVGYGVY
 61 DLYDLGEFNQ KGTVRTKYGT KAQYLQAIQA AHAAGMQVYA DVVFDHKGGA DGTEWVDAVE
121 VNPSDRNQEI SGTYQIQAWT KFDFPGRGNT YSSFKWRWYH FDGVDWDESR KLSRIYKFIG
181 KAWDWEVDTE NGNYDYLMYA DLDMDHPEVV TELKNWGKWY VNTTNIDGFR LDAVKHIKFS
241 FFPDWLSYVR SQTGKPLFTV GEYWSYDINK LHNYITKTNG TMSLFDAPLH NKFYTASKSG
301 GAFDMRTLMT NTLMKDQPTL AVTFVDNHDT EPGQALQSWV DPWFKPLAYA FILTRQEGYP
361 CVFYGDYYGI PQYNIPSLKS KIDPLLIARR DYAYGTQHDY LDHSDIIGWT REGVTEKPGS
421 GLAALITDGP GGSKWMYVGK QHAGKVFYDL TGNRSDTVTI NSDGWGEFKV NGGSVSVWVP
481 RKTT
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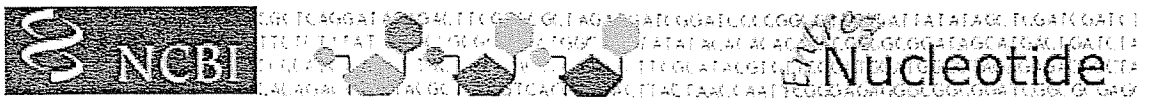
Exhibit 4



1: AF032864. Reports Bacillus stearoth...[gi:2642325] Links

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DEFINITION  Bacillus stearothermophilus alpha amylase (ami) gene, complete cds.
ACCESSION   AF032864
VERSION     AF032864.1  GI:2642325
KEYWORDS    .
SOURCE      Geobacillus stearothermophilus
  ORGANISM  Geobacillus stearothermophilus
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
REFERENCE   1  (bases 1 to 1990)
  AUTHORS   da Silva,A.C.R., Fernandes,E. and Pueyo,M.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-NOV-1997) Physiology, ICB, Av Prof Lineu Prestes, Sao
            Paulo, SP, Brasil
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                     NQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPSDR
                     NQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKA
                     WDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFS
                     FFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK
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                     TEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNG
                     GSVSVWVPRKTTVSTIARPITTRPWTGEFVRWTEPRLVAWP"
ORIGIN
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      121 taacatttga ttaaggggga agggcattgt gctaacgttt caccgcatca ttcgaaaagg
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